

AMERICA

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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/545,334B

DATE: 07/26/2001

TIME: 10:33:53

Input Set : A:\0803.SEQLIST.txt

Output Set: N:\CRF3\07262001\I545334B.raw

#9/K.T.

11-15-01

Raw SEQ  
listing

ENTERED

4 <110> APPLICANT: Zinselmeier, Chris  
5 Habben, Jeff  
6 Tomes, Dwight  
8 <120> TITLE OF INVENTION: Regulated Expression of Genes in Plant  
9 Seeds  
11 <130> FILE REFERENCE: 0803  
13 <140> CURRENT APPLICATION NUMBER: US 09/545,334B  
14 <141> CURRENT FILING DATE: 2000-04-07  
16 <150> PRIOR APPLICATION NUMBER: US 60/129,844  
17 <151> PRIOR FILING DATE: 1999-04-16  
19 <160> NUMBER OF SEQ ID NOS: 12  
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 1608  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Zea mays  
30 <220> FEATURE:  
31 <221> NAME/KEY: CDS  
32 <222> LOCATION: (1)...(1605)  
34 <400> SEQUENCE: 1  
35 atg gcg gtg gtt tat tac ctg ctg gcc ggg ctg atc gcc tgc tct 48  
36 Met Ala Val Val Tyr Tyr Leu Leu Ala Gly Leu Ile Ala Cys Ser  
37 1 5 10 15  
39 cat gca cta gcg gca ggc acg ctt gcg ctc gga gaa gat cgc ggc cgt 96  
40 His Ala Leu Ala Ala Gly Thr Leu Ala Leu Gly Glu Asp Arg Gly Arg  
41 20 25 30  
43 ccc tgg cca gcc ttc ctc gcc gcg ctg gcc ttg gac ggc aag ctc cgg 144  
44 Pro Trp Pro Ala Phe Leu Ala Ala Leu Ala Leu Asp Gly Lys Leu Arg  
45 35 40 45  
47 acc gac agc aac gcg acg gcg gcg gcc tcg acg gac ttc ggc aac atc 192  
48 Thr Asp Ser Asn Ala Thr Ala Ala Ser Thr Asp Phe Gly Asn Ile  
49 50 55 60  
51 acg tcg gcg ctc ccg gcg gtc cta tac ccg tcg tcc acg ggc gac 240  
52 Thr Ser Ala Leu Pro Ala Ala Val Leu Tyr Pro Ser Ser Thr Gly Asp  
53 65 70 75 80  
55 ctg gtg gcg ctg ctg agc gcg gcc aac tcc acc ccg ggg tgg ccc tac 288  
56 Leu Val Ala Leu Ser Ala Ala Asn Ser Thr Pro Gly Trp Pro Tyr  
57 85 90 95  
59 acc atc gcg ttc cgc ggc cgc ggc cac tcc ctc atg ggc cag gcc ttc 336  
60 Thr Ile Ala Phe Arg Gly Arg Gly His Ser Leu Met Gly Gln Ala Phe  
61 100 105 110  
63 gcc ccc ggc ggg gtg gtc gtc aac atg gcg tcc ctg ggc gac gcc gcc 384  
64 Ala Pro Gly Gly Val Val Val Asn Met Ala Ser Leu Gly Asp Ala Ala  
65 115 120 125  
67 gcc gcc gcg ccg ccg cgc gtc aac gtg tcc gcg gac ggc cgc tac gtg 432  
68 Ala Ala Ala Pro Pro Arg Val Asn Val Ser Ala Asp Gly Arg Tyr Val  
69 130 135 140

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71	gac	gcc	ggc	ggc	gag	cag	gtg	tgg	atc	gac	gtg	ctg	cgc	gcg	tct	ctg	480
72	Asp	Ala	Gly	Gly	Glu	Gln	Val	Trp	Ile	Asp	Val	Leu	Arg	Ala	Ser	Leu	
73	145				150						155					160	
75	gcg	cgc	ggc	gtg	gcg	ccg	cgc	tcc	tgg	acc	gac	tac	ctc	tac	ctc	acc	528
76	Ala	Arg	Gly	Val	Ala	Pro	Arg	Ser	Trp	Thr	Asp	Tyr	Leu	Tyr	Leu	Thr	
77					165					170					175		
79	gtc	ggc	ggc	acg	ctg	tcc	aac	gca	ggc	atc	agc	ggc	cag	gcg	ttc	cgc	576
80	Val	Gly	Gly		Thr	Leu	Ser	Asn	Ala	Gly	Ile	Ser	Gly	Gln	Ala	Phe	Arg
81					180					185					190		
83	cac	ggc	cca	cag	ata	tct	aac	gtg	ctg	gag	atg	gac	gtt	atc	acc	ggc	624
84	His	Gly	Pro	Gln	Ile	Ser	Asn	Val	Leu	Glu	Met	Asp	Val	Ile	Thr	Gly	
85					195					200					205		
87	cat	ggg	gag	atg	gtg	acg	tgc	tcc	aag	cag	ctg	aac	gcg	gac	ctg	ttc	672
88	His	Gly	Glu	Met	Val	Thr	Cys	Ser	Lys	Gln	Leu	Asn	Ala	Asp	Leu	Phe	
89					210					215					220		
91	gac	gcc	gtc	ctg	ggc	ggg	ctg	ggg	cag	ttc	gga	gtg	atc	acc	cgg	gcc	720
92	Asp	Ala	Val	Leu	Gly	Gly	Leu	Gly	Gln	Phe	Gly	Val	Ile	Thr	Arg	Ala	
93					225					230			235		240		
95	cg	atc	g	cg	gt	g	g	cg	g	cg	g	cg	t	g	gt	cg	768
96	Arg	Ile	Ala	Val	Glu	Pro	Ala	Pro	Ala	Arg	Ala	Arg	Trp	Val	Arg	Leu	
97					245					250			255				
99	gt	tg	ta	cc	ac	cc	tc	gc	gc	tt	ac	g	c	g	cg	ct	816
100	Val	Tyr	Thr	Asp	Phe	Ala	Ala	Phe	Ser	Ala	Asp	Gln	Glu	Arg	Leu	Thr	
101					260					265			270				
103	gc	cc	cg	cc	gg	gg	gc	gc	tc	tt	gg	cc	at	g	ac	tc	864
104	Ala	Pro	Arg	Pro	Gly	Gly	Gly	Gly	Ala	Ser	Phe	Gly	Pro	Met	Ser	Tyr	
105					275					280			285				
107	gt	tg	ga	gg	tc	gt	tt	gt	aa	c	ag	ac	gt	cc	tg	cg	912
108	Val	Glu	Gly	Ser	Val	Phe	Val	Asn	Gln	Ser	Leu	Ala	Thr	Asp	Leu	Ala	
109					290					295			300				
111	aa	ac	gg	tt	tc	cc	ac	g	cc	gt	cc	gc	cc	at	gc	tc	960
112	Asn	Thr	Gly	Phe	Phe	Thr	Asp	Ala	Asp	Val	Ala	Arg	Ile	Val	Ala	Leu	
113					305					310			315		320		
115	gc	gg	g	cg	aa	gc	cc	ac	cc	gt	ta	ac	at	g	cc	ac	1008
116	Ala	Gly	Glu	Arg	Asn	Ala	Thr	Thr	Val	Tyr	Ser	Ile	Glu	Ala	Thr	Leu	
117					325					330			335				
119	aa	ac	ta	ca	g	cc	ac	g	cg	gt	g	ac	c	g	cc	tc	1056
120	Asn	Tyr	Asp	Asn	Ala	Ala	Ala	Ala	Ala	Val	Asp	Gln	Glu	Leu	Ala		
121					340					345			350				
123	tcc	gt	tg	gg	ac	cg	ct	ag	tc	gt	gaa	gg	tt	cc	cg	cg	1104
124	Ser	Val	Leu	Gly	Thr	Leu	Ser	Tyr	Val	Glu	Gly	Phe	Ala	Phe	Gln	Arg	
125					355					360			365				
127	gac	gt	tg	tc	ta	cg	tc	tt	gac	cg	gt	ca	gg	ga	gg	gt	1152
128	Asp	Val	Ser	Tyr	Thr	Ala	Phe	Leu	Asp	Arg	Val	His	Gly	Glu	Glu	Val	
129					370					375			380				
131	gc	ct	ca	ac	aa	ct	gg	tt	gg	cg	gt	cc	ac	cc	t	cc	1200
132	Ala	Leu	Asn	Lys	Leu	Gly	Leu	Trp	Arg	Val	Pro	His	Pro	Trp	Leu	Asn	
133					385					390			395		400		
135	at	tg	tg	cc	cg	tc	cg	at	cc	g	ac	tt	cc	g	cc	tc	1248

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136	Met Phe Val Pro Arg Ser Arg Ile Ala Asp Phe Asp Arg Gly Val Phe			
137	405	410	415	
139	aag ggc atc ttg cag ggc acc gac atc gtc ggc ccg ctc atc gtc tac			
140	Lys Gly Ile Leu Gln Gly Thr Asp Ile Val Gly Pro Leu Ile Val Tyr		1296	
141	420	425	430	
143	ccc ctc aac aaa tcc atg tgg gac gac ggc atg tcg gcg gcg acg ccg			
144	Pro Leu Asn Lys Ser Met Trp Asp Asp Gly Met Ser Ala Ala Thr Pro		1344	
145	435	440	445	
147	tcg gag gac gtg ttc tac gcg gtg tcg ctg ttc tcg tcg gtg gcg			
148	Ser Glu Asp Val Phe Tyr Ala Val Ser Leu Leu Phe Ser Ser Val Ala		1392	
149	450	455	460	
151	ccc aac gac ctg gcg agg ctg cag gag cag aac agg agg atc ctg cgc			
152	Pro Asn Asp Leu Ala Arg Leu Gln Glu Gln Asn Arg Arg Ile Leu Arg		1440	
153	465	470	475	480
155	ttc tgc gac ctc gcc ggg atc cag tac aag acc tac ctg gcg cgg cac			
156	Phe Cys Asp Leu Ala Gly Ile Gln Tyr Lys Thr Tyr Leu Ala Arg His		1488	
157	485	490	495	
159	acg gac cgc agt gac tgg gtc cgc cac ttc ggc gcc gcc gag tgg aat			
160	Thr Asp Arg Ser Asp Trp Val Arg His Phe Gly Ala Ala Glu Trp Asn		1536	
161	500	505	510	
163	cgc ttc gtg gag atg aag aac aag tac gac ccc aag agg ctg ctc tcc			
164	Arg Phe Val Glu Met Lys Asn Lys Tyr Asp Pro Lys Arg Leu Leu Ser		1584	
165	515	520	525	
167	ccc ggc cag gac atc ttc aac tga			
168	Pro Gly Gln Asp Ile Phe Asn		1608	
169	530	535		
172	<210> SEQ ID NO: 2			
173	<211> LENGTH: 535			
174	<212> TYPE: PRT			
175	<213> ORGANISM: Zea mays			
177	<400> SEQUENCE: 2			
178	Met Ala Val Val Tyr Tyr Leu Leu Leu Ala Gly Leu Ile Ala Cys Ser			
179	1	5	10	15
180	His Ala Leu Ala Ala Gly Thr Leu Ala Leu Gly Glu Asp Arg Gly Arg			
181	20	25	30	
182	Pro Trp Pro Ala Phe Leu Ala Ala Leu Ala Leu Asp Gly Lys Leu Arg			
183	35	40	45	
184	Thr Asp Ser Asn Ala Thr Ala Ala Ala Ser Thr Asp Phe Gly Asn Ile			
185	50	55	60	
186	Thr Ser Ala Leu Pro Ala Ala Val Leu Tyr Pro Ser Ser Thr Gly Asp			
187	65	70	75	80
188	Leu Val Ala Leu Leu Ser Ala Ala Asn Ser Thr Pro Gly Trp Pro Tyr			
189	85	90	95	
190	Thr Ile Ala Phe Arg Gly Arg Gly His Ser Leu Met Gly Gln Ala Phe			
191	100	105	110	
192	Ala Pro Gly Gly Val Val Val Asn Met Ala Ser Leu Gly Asp Ala Ala			
193	115	120	125	
194	Ala Ala Ala Pro Pro Arg Val Asn Val Ser Ala Asp Gly Arg Tyr Val			
195	130	135	140	

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196 Asp Ala Gly Gly Glu Gln Val Trp Ile Asp Val Leu Arg Ala Ser Leu  
 197 145 150 155 160  
 198 Ala Arg Gly Val Ala Pro Arg Ser Trp Thr Asp Tyr Leu Tyr Leu Thr  
 199 165 170 175  
 200 Val Gly Gly Thr Leu Ser Asn Ala Gly Ile Ser Gly Gln Ala Phe Arg  
 201 180 185 190  
 202 His Gly Pro Gln Ile Ser Asn Val Leu Glu Met Asp Val Ile Thr Gly  
 203 195 200 205  
 204 His Gly Glu Met Val Thr Cys Ser Lys Gln Leu Asn Ala Asp Leu Phe  
 205 210 215 220  
 206 Asp Ala Val Leu Gly Gly Leu Gly Gln Phe Gly Val Ile Thr Arg Ala  
 207 225 230 235 240  
 208 Arg Ile Ala Val Glu Pro Ala Pro Ala Arg Ala Arg Trp Val Arg Leu  
 209 245 250 255  
 210 Val Tyr Thr Asp Phe Ala Ala Phe Ser Ala Asp Gln Glu Arg Leu Thr  
 211 260 265 270  
 212 Ala Pro Arg Pro Gly Gly Gly Ala Ser Phe Gly Pro Met Ser Tyr  
 213 275 280 285  
 214 Val Glu Gly Ser Val Phe Val Asn Gln Ser Leu Ala Thr Asp Leu Ala  
 215 290 295 300  
 216 Asn Thr Gly Phe Phe Thr Asp Ala Asp Val Ala Arg Ile Val Ala Leu  
 217 305 310 315 320  
 218 Ala Gly Glu Arg Asn Ala Thr Thr Val Tyr Ser Ile Glu Ala Thr Leu  
 219 325 330 335  
 220 Asn Tyr Asp Asn Ala Thr Ala Ala Ala Val Asp Gln Glu Leu Ala  
 221 340 345 350  
 222 Ser Val Leu Gly Thr Leu Ser Tyr Val Glu Gly Phe Ala Phe Gln Arg  
 223 355 360 365  
 224 Asp Val Ser Tyr Thr Ala Phe Leu Asp Arg Val His Gly Glu Glu Val  
 225 370 375 380  
 226 Ala Leu Asn Lys Leu Gly Leu Trp Arg Val Pro His Pro Trp Leu Asn  
 227 385 390 395 400  
 228 Met Phe Val Pro Arg Ser Arg Ile Ala Asp Phe Asp Arg Gly Val Phe  
 229 405 410 415  
 230 Lys Gly Ile Leu Gln Gly Thr Asp Ile Val Gly Pro Leu Ile Val Tyr  
 231 420 425 430  
 232 Pro Leu Asn Lys Ser Met Trp Asp Asp Gly Met Ser Ala Ala Thr Pro  
 233 435 440 445  
 234 Ser Glu Asp Val Phe Tyr Ala Val Ser Leu Leu Phe Ser Ser Val Ala  
 235 450 455 460  
 236 Pro Asn Asp Leu Ala Arg Leu Gln Glu Gln Asn Arg Arg Ile Leu Arg  
 237 465 470 475 480  
 238 Phe Cys Asp Leu Ala Gly Ile Gln Tyr Lys Thr Tyr Leu Ala Arg His  
 239 485 490 495  
 240 Thr Asp Arg Ser Asp Trp Val Arg His Phe Gly Ala Ala Glu Trp Asn  
 241 500 505 510  
 242 Arg Phe Val Glu Met Lys Asn Lys Tyr Asp Pro Lys Arg Leu Leu Ser  
 243 515 520 525  
 244 Pro Gly Gln Asp Ile Phe Asn

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245	530	535	
247	<210> SEQ ID NO: 3		
248	<211> LENGTH: 51		
249	<212> TYPE: DNA		
250	<213> ORGANISM: Artificial Sequence		
252	<220> FEATURE:		
253	<223> OTHER INFORMATION: Synthesized based on sequence from Agrobacterium		
254	tumefaciens		
256	<400> SEQUENCE: 3		
257	caucaucauc augatccac caatggatct acgtcttaatt ttccggccaa c	51	
259	<210> SEQ ID NO: 4		
260	<211> LENGTH: 42		
261	<212> TYPE: DNA		
262	<213> ORGANISM: Artificial Sequence		
264	<220> FEATURE:		
265	<223> OTHER INFORMATION: Synthesized based on sequence from Agrobacterium		
266	tumefaciens		
268	<400> SEQUENCE: 4		
269	cuacuacuac uagtttaactc acattcgaaa tgggtggcct tc	42	
271	<210> SEQ ID NO: 5		
272	<211> LENGTH: 29		
273	<212> TYPE: DNA		
274	<213> ORGANISM: Zea mays		
276	<400> SEQUENCE: 5		
277	catgccatgg cgggtggtta ttacctgct	29	
279	<210> SEQ ID NO: 6		
280	<211> LENGTH: 31		
281	<212> TYPE: DNA		
282	<213> ORGANISM: Zea mays		
284	<400> SEQUENCE: 6		
285	cgggatcc tcatcatcgtt gaagatgtcc t	31	
287	<210> SEQ ID NO: 7		
288	<211> LENGTH: 5622		
289	<212> TYPE: DNA		
290	<213> ORGANISM: Artificial Sequence		
292	<220> FEATURE:		
293	<223> OTHER INFORMATION: Promoter and terminator from Zea mays as found in		
294	Genbank Accession #S78780; gene from Agrobacterium		
295	tumefaciens as found in Molecular and General		
296	Genetics 216:388-394 (1989).		
298	<400> SEQUENCE: 7		
299	gctctagatt atataattta taagctaaac aaccggccc taaagcacta tcgtatcacc	60	
300	tatctaaata agtcacggga gtttcgaacg tccacttcgt cgcacggaaat tgcatgtttc	120	
301	ttgttggaaag catattcagc caatctccac acataaaagggt ttatgtataa acttacattt	180	
302	agtcagttt aattacagtc ttatgttgc gcatatgtat gtttctcaat ccatataaagt	240	
303	tagagtaaaa aataagttta aattttatct taattcactc caacatataat ggatctacaa	300	
304	tactcatgtg catccaaaca aactacttat attgaggtga atttggtaga aattaaacta	360	
305	acttacacac taagccaatc ttactatata taaagccacca gtttcaacga tcgtcccgcg	420	
306	tcaatattat taaaaactc ctacatttct ttataatcaa cccgcactct tataatctct	480	

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